Amendments to the Specification:

Please replace the existing title at page 1, line 2 with the following rewritten title:

GENES ENCODING STEROL DELTA-14 ~~15~~ REDUCTASE IN PLANTS.

Please replace the paragraph beginning at page 4, lines 25 to 27 with the following rewritten paragraph:

Figures 1A and 1B shows a comparison of the amino acid sequences encoded by a corn and two soybean sterol delta-14 reductase cDNAs (SEQ ID NOs:4, 6, and 8, respectively), and the *Arabidopsis thaliana* sequence (SEQ ID NO:10) that is the closest BLAST homolog.

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Please replace the paragraph beginning at page 8, line 28 and ending at page 9, line 13 with the following rewritten paragraph:

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol.* *215*:403-410~~; see also www.ncbi.nlm.nih.gov/BLAST/~~). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more

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contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that comprise one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

Please replace the paragraph beginning at page 21, line 28 and ending at page 22, line 7 with the following rewritten paragraph:

cDNA clones encoding sterol delta-14 reductase were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410~~; see also www.ncbi.nlm.nih.gov/BLAST/~~) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish and States (1993) *Nat. Genet. 3*:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained

in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.

Please replace the paragraph beginning at page 23, lines 22 and ending at page 24, line 2 with the following rewritten paragraph:

Figures 1A and 1B presents an alignment of the amino acid sequences set forth in SEQ ID NOs:4, 6, and 8, and the *Arabidopsis thaliana* sequence (SEQ ID NO:10). The data in Table 5 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:2, 4, 6, and 8, and the *Ascobolus immersus* and the *Arabidopsis thaliana* sequences (SEQ ID NOs:9 and 10). The nucleotide and polypeptide sequences contained in SEQ ID NOs:1 and 2, respectively, were part of the provisional filing of this application (U.S. Provisional Application No. 60/156820, filed September 30, 1999). The closest art at the time of the provisional filing was the *Ascobolus immersus* enzyme. The *Arabidopsis* Genbank submission is dated July 5, 2000. The percent identity of SEQ ID NO:2 to the *Arabidopsis thaliana* sequence (SEQ ID NO:10, Jang et al. (2000) *Genes Dev. 14*:1485-1497) is 64.3%.